In the Claims

Applicant has submitted a new complete claim set showing marked up claims with insertions indicated by underlining and deletions indicated by strikeouts and/or double bracketing.

Please amend pending claims 1, 3, 11, 14, and 26 as noted below.

Please cancel claims 2, 24, and 28 without prejudice or disclaimer.

1. (Currently Amended) A method for haplotyping, comprising:

analyzing a first polymorphic locus of a nucleic acid within a sample by specifically capturing the nucleic acid on a surface wherein the step of capturing the nucleic acid on the surface identifies only a first allele of a first SNP of the polymorphic locus,

analyzing a second allele of the first SNP of the polymorphic locus by specifically capturing the nucleic acid on a surface wherein the step of capturing the nucleic acid on the surface identifies only the second allele of the first SNP of the polymorphic locus,

wherein the nucleic acid is captured by hybridization with an ASO,

separately analyzing a second SNP of a polymorphic locus of the captured nucleic acid ~~sample~~ by hybridization of the nucleic acids with labeled ASOs from solution to identify both alleles of the second SNP, and

determining the haplotype based on the identification of each allele of each SNP.

2. (Cancelled)

3. (Currently Amended) The method of claim 1, wherein the ASO used to capture the nucleic acid for analysis of the first SNP is fixed to a surface.

4. (Original) The method of claim 3, wherein a first ASO complementary to a first allele of the first SNP and a second ASO complementary to a second allele of the first SNP are hybridized to the surface and are used to capture the nucleic acid.

5. (Original) The method of claim 1, wherein the surface is a multiwell dish.

6. (Original) The method of claim 1, wherein the surface is a chip.

7. (Original) The method of claim 1, wherein the surface is a slide.

8. (Original) The method of claim 1, wherein the surface is a bead.

9. (Original) The method of claim 4, wherein each ASO corresponding to an allele of the first SNP further includes a spacer sequence.

10. (Original) The method of claim 9, wherein the spacer sequence is selected from the group consisting of a poly-T, poly-A, poly-C, and poly-G.

11. (Currently Amended) The method of claim ~~2~~ 1, wherein the second SNP is analyzed by hybridization of the nucleic acid sample with an ASO complementary to a first allele of the second SNP and an ASO complementary to a second allele of the second SNP.

12. (Original) The method of claim 11, wherein each of the ASOs corresponding to an allele of the second SNP is hybridized independently to the nucleic acid sample.

13. (Original) The method of claim 11, wherein at least one of the ASOs complementary to an allele of the first SNP and at least one of the ASOs complementary to an allele of the second SNP contains a fluorescent label or quencher, the fluorescent label or quencher of the two ASOs, being distinct from one another.

14. (Currently Amended) The method of claim ~~2~~ 1, wherein the alleles of the second SNP are analyzed simultaneously with one another.

15. (Original) The method of claim 1, wherein each of the ASOs complementary to an allele of the first SNP and each of the ASOs complementary to an allele of the second SNP contains a

fluorescent label or quencher, the fluorescent label or quencher of each of the four ASOs, being distinct from one another.

16. (Original) The method of claim 1, wherein the nucleic acid sample is prepared by PCR amplification of a polymorphic locus from a genomic DNA sample.

17. (Original) The method of claim 1, wherein the nucleic acid sample is a reduced complexity genome.

18. (Original) The method of claim 1, wherein the nucleic acid sample is labeled with a first label.

19. (Original) The method of claim 1, wherein the presence of one set of alleles at the polymorphic locus is associated with a disease and the haplotyping method is performed to identify predisposition to the disease.

20. (Original) The method of claim 1, further comprising analyzing a third SNP of a polymorphic locus of the nucleic acid sample to identify both alleles of the third SNP, and determining the haplotype based on the identification of each allele of each SNP.

21. (Original) The method of claim 1, further comprising analyzing a fourth SNP of a polymorphic locus of the nucleic acid sample to identify both alleles of the fourth SNP, and determining the haplotype based on the identification of each allele of each SNP.

22. (Original) The method of claim 1, wherein the analysis of the first and second SNPs are performed simultaneously.

23-24. (Cancelled)

25. (Original) The method of claim 1, wherein the nucleic acid sample is an RNA genome.

26. (Currently Amended) The method of claim ~~1~~ 25, wherein the RNA genome is made from cDNA.

27. (Original) The method of claim 1, wherein the nucleic acid sample is genomic DNA.

28-64. (Cancelled)

65. (Previously presented) The method of claim 1, wherein the haplotype comprises an ordered combination of alleles in a defined genetic region that co-segregates.